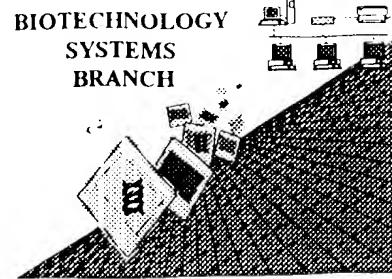


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/727,855A
Source: 1645
Date Processed by STIC: 6/7/2001

RECEIVED

JUN 27 2001

TECH CENTER 1600/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

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JUN 27 2001

Raw Sequence Listing Error Summary

TECH CENTER 2000

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/122,855A</u>
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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/727,855A

DATE: 06/07/2001
TIME: 14:25:41

Input Set : A:\SeqListing.txt
Output Set: C:\CRF3\06072001\I727855A.raw

P. 6

3 <110> APPLICANT: F. HOFFMANN-LA ROCHE AG
5 <120> TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND
6 BIOLOGICALLY USEFUL MATERIALS THEREOF
8 <130> FILE REFERENCE: SOD
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/727,855A
C--> 11 <141> CURRENT FILING DATE: 2000-12-01
13 <150> PRIOR APPLICATION NUMBER: EP99123821.3
14 <151> PRIOR FILING DATE: 1999-12-01
16 <160> NUMBER OF SEQ ID NOS: 17
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3632
22 <212> TYPE: DNA
23 <213> ORGANISM: Phaffia rhodozyma
25 <220> FEATURE:
26 <221> NAME/KEY: 5'UTR
27 <222> LOCATION: (922)..(923)
28 <223> OTHER INFORMATION: EXPERIMENTAL
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32 <222> LOCATION: (986)..(1096)
34 <220> FEATURE:
35 <221> NAME/KEY: intron
36 <222> LOCATION: (1097)..(1306)
38 <220> FEATURE:
39 <221> NAME/KEY: exon
40 <222> LOCATION: (1307)..(1456)
42 <220> FEATURE:
43 <221> NAME/KEY: intron
44 <222> LOCATION: (1457)..(1555)
46 <220> FEATURE:
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48 <222> LOCATION: (1556)..(1589)
50 <220> FEATURE:
51 <221> NAME/KEY: intron
52 <222> LOCATION: (1590)..(1694)
54 <220> FEATURE:
55 <221> NAME/KEY: exon
56 <222> LOCATION: (1695)..(1799)
58 <220> FEATURE:
59 <221> NAME/KEY: intron
60 <222> LOCATION: (1800)..(1920)
62 <220> FEATURE:
63 <221> NAME/KEY: exon
64 <222> LOCATION: (1921)..(1982)
66 <220> FEATURE:
67 <221> NAME/KEY: intron

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/727, 855A

DATE: 06/07/2001

TIME: 14:25:41

Input Set : A:\SeqListing.txt
 Output Set: C:\CRF3\06072001\I727855A.raw

68 <222> LOCATION: (1983)..(2076)
 70 <220> FEATURE:
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 72 <222> LOCATION: (2077)..(2140)
 74 <220> FEATURE:
 75 <221> NAME/KEY: intron
 76 <222> LOCATION: (2141)..(2246)
 78 <220> FEATURE:
 79 <221> NAME/KEY: exon
 80 <222> LOCATION: (2247)..(2272)
 82 <220> FEATURE:
 83 <221> NAME/KEY: intron
 84 <222> LOCATION: (2273)..(2390)
 86 <220> FEATURE:
 87 <221> NAME/KEY: exon
 88 <222> LOCATION: (2391)..(2507)
 90 <220> FEATURE:
 91 <221> NAME/KEY: polyA_site
 92 <222> LOCATION: (2663)..(2664)
 93 <223> OTHER INFORMATION: EXPERIMENTAL
 95 <400> SEQUENCE: 1
 96 tcctgtttagt aatctttcta acgccttgtta ctttgaccata ggcgtttgtc cgaaattttg 60
 98 caaaacttagt gttggcgeca tggacggcttc tcggatccag aactgacggc tcgcacaataa 120
 100 agtatgacga tggtagaggt gaaggaggaa accacaggtt gaccagtctc aaagagtgtct 180
 102 gatgtgcgcg aggatttgctc attaaatgtt gtttatatgt cttaggccaa gagaagacat 240
 104 ttggttttgg ttttgggttt gcatttgatg agatgtgtca cgattgaaga cgggaggagg 300
 106 ctcacttaacc caagaagccca ggatcaggag gaatgcctcc cccttttcat caagatcttt 360
 108 ctcacatcgca acatttgaca ttctcttttag tatcccttcta tccttttctt ccaacttctc 420
 110 ccattgtatc gactttgtc gacttgctct tcttatctct gagcagagat gggcattcca 480
 112 atatcgaagg agcgcacacaa gaccttggag tttggtaac agatgaagag gggccggaggt 540
 114 ggatggggct gttagaaagta gctgatecat gatgttctgg atgatgatag gcgaaggAAC 600
 116 agacatagga tctctgtctc gtccttggat tactgagtct tttatccagc gtgttctttgt 660
 118 ctgcagaagaag ctttcaagat cgatgtaa taagacaggc aatgaggacg gaccaacgaa 720
 120 cgaacgaaaaa gaacagaaga gctggtaagt cagtcagtca gtcagtcaatgtaatcaaaaca 780
 122 ctgggtgttata gggttatagc tcgacgcgcac ggcgcgcgtt tgagacgcga tatgttttacg 840
 124 taatacctgg cgtcatcccc ccagccggagg caagagccga gccgctctg aacgacaaaaa 900
 126 ttc当地tccatc ttaagctcat tctcatctaa ccgactcatc tc当地ccat 960
 128 catccccatc attctacccgc catcc atg tct gtt cga gca tcc ctc tct tcc 1012
 130 gtt tct aga cag act ttc gtc gct cct gct get ttc cag atc agg gca 1060
 132 aag cat acc ctg cct gag ctt cct tac get tac gat gtaagacttt 1106
 134 tcctgtttctc cttatctgtc gctttttgg ttttttctgt ctccgcctc tagctttct 1166
 136 tggcttcttc tggctgtc tttgttggat atattcagct cgatagacta acccatctca 1226
 138 tctctggac attctttac tggaaacgta tcttgcctt ggtttttctt ggcttgggtt 1286
 140 gaaaattctt ctccactcag gcc ctg gag ccc tcc atc tcc aag gag atc atg 1339
 142 acc ctt cac cac acc aag cac cat cag act tat gtt aac ggc ctc aac 1387
 144 gct gcc gag gag agc tac tgg gtc gct gtt ggc aag gag gat gtt ctt 1435
 146 acc cag gtt aag ctt cag tct gtacgtctga ccgtttttt atcgaccgga 1486
 148 acgcctggtg aggagggaga tgaagtttga tgagcgtca tcgtctagca cgttgaccgg 1546
 150 atcatacag gct ctc aag ttc aac gga gga gga cac atc aat c 1589

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/727,855A

DATE: 06/07/2001

TIME: 14:25:41

Input Set : A:\SeqListing.txt
Output Set: C:\CRF3\06072001\R727855A.raw

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/727,855A

DATE: 06/07/2001

TIME: 14:25:41

Input Set : A:\SeqListing.txt
Output Set: C:\CRF3\06072001\I727855A.raw

241 <222> LOCATION: (1064)..(1237)
243 <220> FEATURE:
244 <221> NAME/KEY: exon
245 <222> LOCATION: (1238)..(1280)
247 <220> FEATURE:
248 <221> NAME/KEY: intron
249 <222> LOCATION: (1281)..(1358)
251 <220> FEATURE:
252 <221> NAME/KEY: exon
253 <222> LOCATION: (1359)..(1402)
255 <220> FEATURE:
256 <221> NAME/KEY: intron
257 <222> LOCATION: (1403)..(1483)
259 <220> FEATURE:
260 <221> NAME/KEY: exon
261 <222> LOCATION: (1484)..(1589)
263 <220> FEATURE:
264 <221> NAME/KEY: intron
265 <222> LOCATION: (1590)..(1674)
267 <220> FEATURE:
268 <221> NAME/KEY: exon
269 <222> LOCATION: (1675)..(1826)
271 <220> FEATURE:
272 <221> NAME/KEY: intron
273 <222> LOCATION: (1827)..(1907)
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276 <221> NAME/KEY: exon
277 <222> LOCATION: (1908)..(1922)
279 <220> FEATURE:
280 <221> NAME/KEY: intron
281 <222> LOCATION: (1923)..(1992)
283 <220> FEATURE:
284 <221> NAME/KEY: exon
285 <222> LOCATION: (1993)..(2056)
287 <220> FEATURE:
288 <221> NAME/KEY: intron
289 <222> LOCATION: (2057)..(2131)
291 <220> FEATURE:
292 <221> NAME/KEY: exon
293 <222> LOCATION: (2132)..(2157)
295 <220> FEATURE:
296 <221> NAME/KEY: intron
297 <222> LOCATION: (2158)..(2238)
299 <220> FEATURE:
300 <221> NAME/KEY: exon
301 <222> LOCATION: (2239)..(2293)
303 <220> FEATURE:
304 <221> NAME/KEY: intron
305 <222> LOCATION: (2294)..(2376)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/727,855A

DATE: 06/07/2001

TIME: 14:25:41

Input Set : A:\SeqListing.txt
Output Set: C:\CRF3\06072001\R727855A.raw

307 <220> FEATURE:
308 <221> NAME/KEY: exon
309 <222> LOCATION: (2377)..(2426)
311 <220> FEATURE:
312 <221> NAME/KEY: intron
313 <222> LOCATION: (2427)..(2524)
315 <220> FEATURE:
316 <221> NAME/KEY: exon
317 <222> LOCATION: (2525)..(2542)
319 <220> FEATURE:
320 <221> NAME/KEY: polyA_site
321 <222> LOCATION: (2667)..(2668)
322 <223> OTHER INFORMATION: EXPERIMENTAL
324 <400> SEQUENCE: 2
325 ctatcccttc tgccgtggc ctgtgtctgt cgagtgtgtg ggatggttt ggataatgttc 60
327 ctatacgaaa ggttagcgac agcaaaagctg acagtattaa gcaagacaag agcttcttcc 120
329 tggcacaga taaaaggacg aactatgaag ctgtccatgc tccccaaacc gattgacaca 180
331 ccgcgcgtca gcaacgcaga atttctcaact gcttcgacgt cacaccaaca tcgatccctcc 240
333 atacctaaaa gcaagatcgag acacattgtt ggtcggcatg ttggatggat gtacatcaaa 300
335 cccacagcat atatcaactca catgtgagaa ctccgtagcc tctaccttct tgcgtctcaa 360
337 tctgaatgtc tggatggag gtggaatgaa tggatcacgt ttgagaagac gaaagaaaaga 420
339 aagagaagag aagagaggaa taogtacgac gaagttatca tcgtatggga acttttctaa 480
341 aaaactgcct atagtagagaa cgtatctctgg agggaaagctc tggatgtatga tagtgaagag 540
343 cgagcaagtc tggcaagtg catttcgtctc ctacaagaaa gagaccaggaa aatgaaggag 600
345 agacgagtaa gcaggtacatcc accgatattt gatcgttctc tctaccgc gatgccttca 660
347 ccaacgcgttc tatctttct tggatggca gatacatact taacgagagc aatctgtatgt 720
349 ataccgaact tggaaacggaa tggatcccaga atcccttga acccttgaac ccttgaaccc 780
351 tggaaaccaag taccaaccga gcaacacgc gatacgtcc acaccacaga accacacgccc 840
353 ctcgtcatta aagggtggac ggcgcgtatgc tggatcacgtt cggcccaatc cgaaagttac 900
355 cggtttggac gtgcgtgtaa ccatgcctgt acggatattt gccttcagct aactccatct 960
357 catcttttcc ttttactacc acaacccacc cttgaacctt cttcccccggc ttttttacta 1020
359 tatccatcta tcaatcatc atg gct cct tac act ctt ccc gac gtaagctaa 1073
361 agtttgagct gtgtgtgtt atctcaatct tggatggaa ctcaccgttt tttttttttt 1133
363 cttccctgggtt tttttatcgg catccctccct ttttttcccc tcgtggtcgc atatgatttg 1193
365 ctcatcaatc gggtttccccc atgcattttt gtcattccgtt tcag ctt cct tac gct 1249
367 tac gat gcc ttg gag cct tac atc tct aag g gtgagattct tagtcagact 1300
369 gttgttccgg ttcgacacacgaa tagtaatcg tctctgttc ctcaatatga acatgcag 1358
371 aa atc atg atc ctt cac cac aag cac cat cag act tac gtc 1402
373 gtacgttaatc taaagggtcat ctccgtctac atggccggat caacttgctc atagatcttcc 1462
375 cttctgttccg ggcgtacgta g acc aac ctc aac gcc gct atc cag gct ttc 1513
377 tcc cag acc aat gac atc aag gcc cag atc gct ctt cag agc gct ctc 1561
379 aag ttc aac gga gga gga cac atc aac c gtacgtatcat tctcccttt 1609
381 ctggcttatac atatgtgttg ctgtgtacta acacgcgtac aaccccggttatctcaccc 1669
383 tgttag ac tcc ctc ttc tgg aag aac atg gct cct gcc gac tct gct gat 1718
385 gcc aag ctc acc gag gga tgg ctc aag act gcc atc gac aag gac ttt 1766
387 gga tcc ttc gag gag ttc aag aag aag ttc aac act gct act ctc ggt 1814
389 gtc cag gga tct gtcgtatct cgtttgttc gacatactct cagctttccct 1866
391 tcgcgtaaact gacgaatagt ttttggaca tggatgtatc g gga tgg gga tgg ctc 1922
393 atqcqtttqa ctttttcca cttqaacat taqcqataqt qataccta aactgtgaat 1982

1/727,855A 6

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sod1 (sense
primer for cloning of SOD genes)

<400> 10
aarcaycayc aracn~~t~~aygt naa

see item 9 on Error Summary Sheet

23

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sod4 (antisense
primer for cloning of SOD genes)

<400> 11
gcccancncng anccytgnac ncc
↓ item 9

23

The types of errors shown exist throughout the Sequence Listing. Please check
subsequent sequences for similar errors.

VERIFICATION SUMMARYPATENT APPLICATION: **US/09/727,855A**

DATE: 06/07/2001

TIME: 14:25:42

Input Set : A:\SeqListing.txt
Output Set: C:\CRF3\06072001\I727855A.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:881 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:881 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:894 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:894 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:963 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:963 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:976 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:976 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17